



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No: 09/972,268  
Applicants: Peter R. Baum, William C. Fanslow III, Timothy E. Lofton,  
Eric A. Sorensen, and Adel Youakim  
Filed: October 5, 2001  
Title: NECTIN POLYPEPTIDES  
  
TC/Art Unit: 1644  
Examiner: Maher M. Haddad  
  
Docket No.: 3101-A

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

**DECLARATION UNDER 37 C.F.R. § 1.131**

We, Peter R. Baum, William C. Fanslow III, Timothy E. Lofton, Eric A. Sorensen, and Adel Youakim, the undersigned, hereby declare that:

1. This Declaration is made by the inventors of the above-captioned patent application in order to establish a date of invention in the United States prior to April 1, 2000.
2. Prior to April 1, 2000, a DNA clone that encodes human nectin-3 polypeptide (also called "B7L4" polypeptide) had been isolated and its sequence determined in the United States by inventors named in the subject application, as evidenced by the Exhibits A and B enclosed herewith. The works described in Exhibits A and B were completed in this country prior to April 1, 2000.
3. Exhibit A is a copy of a page from one of the laboratory notebooks of Eric A. Sorensen, written in his handwriting, describing a restriction enzyme digest of an isolated lambda phage clone called "HuB7L4 11-1". All dates on the copy have been redacted.

4. Exhibit B (eight pages) is a copy of a computer printout that is incorporated into one of the laboratory notebooks of Eric A. Sorensen, showing the results of the sequencing of the HuB7L4 11-1 clone insert that was performed at the direction of Eric A. Sorensen. The amino acid sequence shown below the corresponding nucleotide sequences is that of human nectin-3 as presented in SEQ ID NO:2 of the above-captioned application (and is identical to amino acids 8 through 549 of SEQ ID NOs 4 and 6). The first page of Exhibit B indicates the location of a predicted signal sequence cleavage site, and the fourth page of Exhibit B indicates the location of the start of the transmembrane domain. All dates on the copy have been redacted.

5. Therefore, on a date prior to April 1, 2000, the inventors of the above-captioned application had determined the amino acid sequence of a human nectin-3 polypeptide including the extracellular domain of a mature form of human nectin-3.

6. As a person signing below: I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

\_\_\_\_\_  
Peter R. Baum

Date: \_\_\_\_\_

\_\_\_\_\_  
William C. Fanslow III  
William C. Fanslow III

Date: June 23, 2003

\_\_\_\_\_  
Timothy E. Lofton  
Timothy E. Lofton

Date: 23 JUNE 2003

\_\_\_\_\_  
Eric A. Sorensen  
Eric A. Sorensen

Date: June 24, 2003

\_\_\_\_\_  
Adel Youakim  
Adel Youakim

Date: June 24, 2003

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Ø DNA for H-B7C4 pulks 11-1 and 13 (from KEB library)  
sat in PEG for the 3 weeks I was on vacation.

Spun out Washed 1x w/ 70% EtOH. Spd vac'd  
out heat. Resuspended o/n in 60 µl H<sub>2</sub>O.

Digest Ø DNAs w/ EcoRI (NEB rxn, buffer) and w/ NotI (NEB buffer, Bst)

1.) Ø DNA 11-1 w/ EcoRI

2.) " " w/ NotI

3.) Ø DNA 13 w/ EcoRI

4.) " " w/ NotI

4 µl Ø DNA

1.5 µl 10x Buffer

.5 µl enzyme

9 µl H<sub>2</sub>O

37°C 60-90'

# 11-1

Ⓢ

95.5 µg/ml

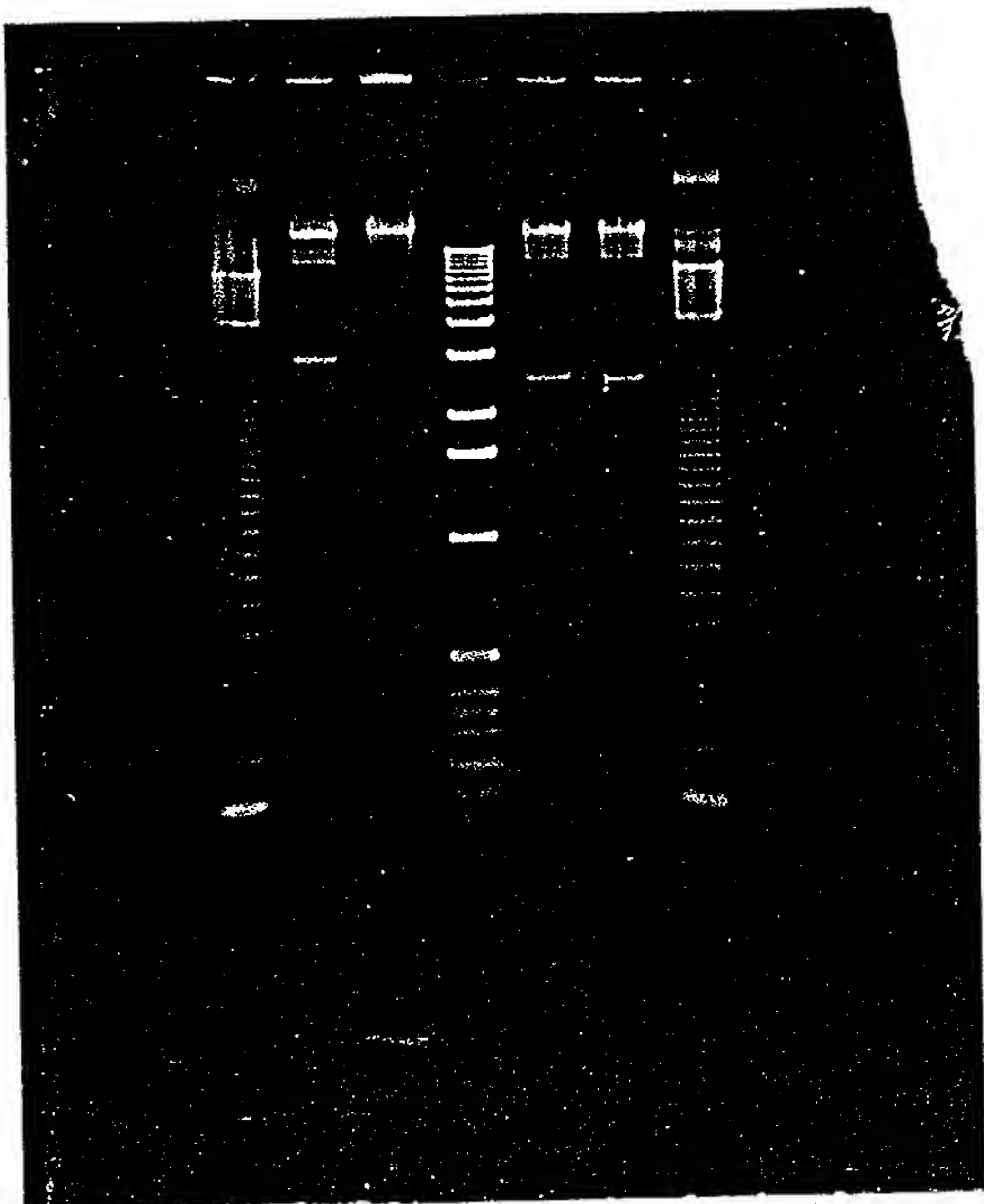
# 13

Ⓢ

57.7 µg/ml

### RESULTS:

According to this gel, the clone  
#13 is way small compared to  
what I estimated by sequence & Pst  
I guess I'll see what the DNA size  
like and I'm going to subclone  
the EcoRI fragment into pBS



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Witnessed & Understood by me,

Date

Invented by

Date

Recorded by

(Linear) (MinSite=6) MAP of: hub714-11.seq check: 8088 from: 1 to: 3187

HuB7L4 #11 from KB library clone #11-1. Phage DNA: **NOT CONFIRMED**

sr6527 R. Sorensen

/bertlesj/sorensen/sr6527/hub714-11.seq

8139,8140,DPC#9117-20,12233-34,12759-60,12801

HuB7L4-11

With 164 enzymes: \*

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                                MspAII
                                BsiEI |
                                EaeI  |
                                EagI  |
                                ApoI  |
                                GdiII |
                                EcoRI  |
                                NotI   |
                                MspAII
                                BpmI

34356-->Sali-GCGGGCATGGCCCGGACCCCGGCCCC-
V-D -A G M A R T P G P
CAAAGAATTTCGCGGCCGCTGTCCCCGCTGTGTCTGAGGCGGCAAAGCACAACTTTCC
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTTTTCTTAAGCGCCGCGACAGGGGCGACACAGGACCTCCGCCGTTTCGTGTTGAAAGG
a
                                S P L C P G G G K A Q L S -

                                BsaXI
                                BanII
                                Bsp1286I
                                PstI
                                BsaHI
                                Hin4I |
                                BseRI  |
                                Hin4I  |
                                SfcI   |
                                BplI   |
                                MspAII |
                                TCCGCTTCTCTCCTCGGAGCCGGGCTCCTGCTGCAGCCCCGACGCCACCTCCGCTGCTG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGGCGAAGAGAGAGCCTCGGCCCGAGGACGACGTCGGGGGCTGCGGTGGAGGCGACGAC
a
                                S A S L L G A G L L L Q P P T P P P L L -

                                MspAII
                                EarI  |
                                SapI   |
                                BpmI   |
                                EarI   |
                                SapI   |
                                AlwNI  |
                                BanI   |
                                BspGI  |
                                (AgeI)

34359 --> ACCGGT-AGGCTCTGTGGTGCCTTAGCTGG 33684 ->
CTGCTGCTCTTCCCGCTGCTGCTCTTCTCCAGGCTCTGTGGTGCCTTAGCTGGACCAATT
121 -----+-----+-----+-----+-----+-----+-----+ 180
GACGACGAGAAGGGCGACGACGAGAAGAGGTCCGAGACACCACGGAATCGACCTGGTTAA
a
                                < 34032 (AP1 rev)
                                L L L F P L L L F S R L C G A L A G P I -
Predicted signal seq. Cleavage ^
                                NspI
                                AflIII
                                BspLU11I
                                MslI
                                ATTGTGGAGCCACATGTCACAGCAGTATGGGGAAAGAATGTTTCATTAAAGTGTTTAATT
181 -----+-----+-----+-----+-----+-----+-----+ 240

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TAACACCTCGGTGTACAGTGTCTCATACCCCTTTCTTACAAAGTAATTTACAAATTAA
      < 34054
a      I V E P H V T A V W G K N V S L K C L I -

      33686 →
GAAGTAAATGAAACCATAACACAGATTTTCATGGGAGAAGATACATGGCAAAAGTTCACAG
241 -----+-----+-----+-----+-----+-----+ 300
CTTCATTTACTTTGGTATTGTGTCTAAAGTACCCTCTTCTATGTACCGTTTTCAAGTGTC
a      E V N E T I T Q I S W E K I H G K S S Q -

      XcmI      AhoI      EarI
      |      |      |
ACTGTTGCAGTTCACCATCCCCAATATGGATTCTCTGTTCAAGGAGAATATCAGGGAAGA
301 -----+-----+-----+-----+-----+-----+ 360
TGACAACGTCAAGTGGTAGGGGTATACCTAAGAGACAAGTTCCTCTTATAGTCCCTTCT
      < 33685
a      T V A V H H P Q Y G F S V Q G E Y Q G R -

      DraI
      |
GTCTTGTTTAAAAATTACTCACTTAATGATGCAACAATTACTCTGCATAACATAGGATTC
361 -----+-----+-----+-----+-----+-----+ 420
CAGAACAAATTTTAAATGAGTGAATTACTACGTTGTTAATGAGACGTATTGTATCCTAAG
a      V L F K N Y S L N D A T I T L H N I G F -

      BmrI
      |
TCTGATTCTGGAAAATACATCTGCAAAGCTGTTACATTCCCGCTTGGAAATGCCAGTCC
421 -----+-----+-----+-----+-----+-----+ 480
AGACTAAGACCTTTTATGTAGACGTTTCGACAATGTAAGGGCGAACCTTTACGGGTCAGG
      < 33687
a      S D S G K Y I C K A V T F P L G N A Q S -

TCTACAACTGTAAGTGTGTTAGTTGAACCCACTGTGAGCCTGATAAAAGGGCCAGATTCT
481 -----+-----+-----+-----+-----+-----+ 540
AGATGTTGACATTGACACAATCAACTTGGGTGACACTCGGACTATTTTCCCGGTCTAAGA
a      S T T V T V L V E P T V S L I K G P D S -

      AlwNI
      |
TTAATTGATGGAGGAAATGAAACAGTAGCAGCCATTTGCATCGCAGCCACTGGAAAACCC
541 -----+-----+-----+-----+-----+-----+ 600
AATTAACCTACCTCCTTTACTTTGTTCATCGTCGGTAAACGTAGCGTCGGTGACCTTTTGGG
a      L I D G G N E T V A A I C I A A T G K P -

      BmrI
      |
32121 →
GTTGCACATATTGACTGGGAAGGTGATCTTGGTGAAATGGAATCCACTACAACCTCTTTT
601 -----+-----+-----+-----+-----+-----+ 660
CAACGTGTATAACTGACCCTTCCACTAGAACCCTTTACCTTAGGTGATGTTGAAGAAA
      < 33688
a      V A H I D W E G D L G E M E S T T T S F -

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                                TatI
                                |
CCAAATGAAACGGCAACGATTATCAGCCAGTACAAGCTATTTCCAACCAGATTGCTAGA
661 -----+-----+-----+-----+-----+-----+-----+ 720
GGTTTACTTTGCCGTTGCTAATAGTCGGTCATGTTTCGATAAAGGTTGGTCTAAACGATCT
a   P N E T A T I I S Q Y K L F P T R F A R -

                                MmeI          BsbI          StyI
                                |          |          |
GGAAGGCGAATTACTTGTGTTGTAAAACATCCAGCCTTGGAAAAGGACATCCGATACTCT
721 -----+-----+-----+-----+-----+-----+-----+ 780
CCTTCCGCTTAATGAACACAACATTTTGTAGGTCGGAACCTTTTCCTGTAGGCTATGAGA
                                ← 32122
a   G R R I T C V V K H P A L E K D I R Y S -

                                Eco57I
                                |
TTCATATTAGACATACAGTATGCTCCTGAAGTTTCGGTAACAGGATATGATGGAAATTGG
781 -----+-----+-----+-----+-----+-----+-----+ 840
AAGTATAATCTGTATGTCATACGAGGACTTCAAAGCCATTGTCCTATACTACCTTTAACC
a   F I L D I Q Y A P E V S V T G Y D G N W -

                                BsaBI          MmeI
                                |          |
TTTGTAGGAAGAAAAGGTGTTAATCTCAAATGTAATGCTGATGCAAATCCACCACCCTTC
841 -----+-----+-----+-----+-----+-----+-----+ 900
AAACATCCTTCTTTTCCACAATTAGAGTTTACATTACGACTACGTTTAGGTGGTGGGAAG
a   F V G R K G V N L K C N A D A N P P P F -

                                Eco57I
                                |
BspMI          HaeI          |
|          |          |
AAATCTGTGTGGAGCAGGTTGGATGGACAATGGCCTGATGGTTTATTGGCTTCAGACAAT
901 -----+-----+-----+-----+-----+-----+-----+ 960
TTTAGACACACCTCGTCCAACCTACCTGTTACCGGACTACCAAATAACCGAAGTCTGTTA
a   K S V W S R L D G Q W P D G L L A S D N -

                                EarI
                                |
ACTCTTCATTTTGTCCATCCATTGACTTTCAATTATTCTGGTGTATTATCTGTAAAGTG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TGAGAAGTAAACAGGTAGGTAAGTAAAGTAAATAAGACCACAAATATAGACATTTTAC
a   T L H F V H P L T F N Y S G V Y I C K V -

                                StyI          DrdI          BstYI Eco57I
                                |          |          |          |
ACCAATTCCTTGGTCAAAGAAGTGACCAAAAAGTCATCTACATTTTCAGATCCTCCTACT
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
TGGTTAAGGGAACCAGTTTCTTCACTGGTTTTTCAGTAGATGTAAAGTCTAGGAGGATGA
a   T N S L G Q R S D Q K V I Y I S D P P T -

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                                BstYI
                                |
ACTACCACCCTTCAGCCTACAATTCAGTGGCATCCCTCAACTGCTGACATCGAGGATCTA
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
TGATGGTGGGAAGTCGGATGTAAAGTCACCGTAGGGAGTTGACGACTGTAGCTCCTAGAT
a   T T T L Q P T I Q W H P S T A D I E D L -

                                HincII
                                |
GCAACAGAACCTAAAAAATTGCCCTTCCCATTTGTCAACTTTGGCAACAATTAAGGATGAC
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
CGTTGTCTTGGATTTTTTTAACGGGAAGGGTAACAGTTGAAACCGTTGTAAATTCCTACTG
a   A T E P K K L P F P L S T L A T I K D D -

                                ScaI
                                |
                                |
                                |
MunI      TaqII      BanII      TatI
|          |          |          |
|          |          |          |
|          |          |          |
ACAATTGCCACGATCATTGCTAGTGTAGTGGGTGGGGCTCTCTTCATAGTACTTGTAAGT
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
TGTTAACGGTGCTAGTAACGATCACATCACCCACCCCGAGAGAAGTATCATGAACATTCA
TGTTAACGGTGC-TCTAGA ←32124
Start Transmembrane ^ <--34357
a   T I A T I I A S V V G G A L F I V L V S -

                                Bsp24I
                                |
                                |
                                |
                                |
                                |
                                |
SspI      SfcI      BbsI      Bsp24I
|          |          |          |
|          |          |          |
|          |          |          |
GTTTTGGCTGGAATATTCTGCTATAGGAGAAGACGGACGTTTCGTGGAGACTACTTTGCC
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
CAAAACCGACCTTATAAGACGATATCCTCTTCTGCCTGCAAAGCACCTCTGATGAAACGG
a   V L A G I F C Y R R R R T F R G D Y F A -

AAGAACTACATTCCACCATCAGATATGCAAAAAGAATCACAAATAGATGTTCTTCAACAA
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
TTCTTGATGTAAGGTGGTAGTCTATACGTTTTTCTTAGTGTTTATCTACAAGAAGTTGTT
← 32125
a   K N Y I P P S D M Q K E S Q I D V L Q Q -

GATGAGCTTGATTCTTACCCAGACAGTGTAAGAAAAGAAAACAAAATCCAGTGAACAAT
1381 -----+-----+-----+-----+-----+-----+-----+ 1440
CTACTCGAACTAAGAATGGGTCTGTACATTTTTTTCTTTTGTGTTTGTAGGTCACCTTGTTA
a   D E L D S Y P D S V K K E N K N P V N N -

BsaAI      EarI
SnaBI      SapI
|          |
|          |
CTAATACGTAAAGACTATTTAGAAGAGCCTGAAAAAACTCAGTGGAACAATGTAGAAAAT
1441 -----+-----+-----+-----+-----+-----+-----+ 1500
GATTATGCATTTCTGATAAATCTTCTCGGACTTTTTTGTAGTCACCTTGTTACATCTTTTA
a   L I R K D Y L E E P E K T Q W N N V E N -

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                                BglIII
                                BstYI
                                |
CTCAATAGGTTTGAAGACCAATGGATTATTATGAAGATCTAAAAATGGGAATGAAGTTT
1501 -----+-----+-----+-----+-----+-----+ 1560
GAGTTATCCAACTTTCTGGTTACCTAATAATACTTCTAGATTTTACCCTTACTTCAA
a  L N R F E R P M D Y Y E D L K M G M K F -

                                MslI
                                NspI
                                |
                                AflIII
                                BspLU11I
                                |
                                MslI
                                |
                                DrdII
                                |
GTCAGTGATGAACATTATGATGAAAACGAAGATGACTTAGTTTCACATGTAGATGGTTCC
1561 -----+-----+-----+-----+-----+-----+ 1620
CAGTCACTACTTGTAATACTACTTTTGCTTCTACTGAATCAAAGTGACATCTACCAAGG
a  V S D E H Y D E N E D D L V S H V D G S -

                                BsrGI
                                TatI
                                |
                                (NotI)
                                |
GTAATTTCCAGGAGGGAGTGGTATGTTTAGCAACCACTGAATGTGACTTAACTATGTACA
1621 -----+-----+-----+-----+-----+-----+ 1680
CATTAAAGGTCCTCCCTCACCATACAAATCGTTGGTGACTTACACTGAATTGATACATGT
a  V I S R R E W Y V * <--34358 -CGCCGGCG <--36018

                                SpeI
                                BclI
                                |
                                SmlI
                                |
ATGTTTCATTCACACTAGTTGATCATTTCAGATTGTTTCATACTTTTCTTGAGGAAGAAT
1681 -----+-----+-----+-----+-----+-----+ 1740
TACAAGTAAGTGTGATCAACTAGTAAAAGTCTAACAAGTATGAAAAAGAACTCCTTCTTA

HindIII  Bce83I  HindIII
|          |          |
AAGCTTTTTCAAGTTGATTTTCAAGCTTACTTTTTATATTCTAATCTGACAAATGAAAAT
1741 -----+-----+-----+-----+-----+-----+ 1800
TTCGAAAAAGTTCAACTAAAAGTTCGAATGAAAAATATAAGATTAGACTGTTTACTTTTA

                                TatI
                                Bce83I
                                |
                                |
GTAAAATCTGAGTTCAGTGTATCTAAGCTGCTTTACAATTTTTTTTCAATGCTGTACTAC
1801 -----+-----+-----+-----+-----+-----+ 1860
CATTTTAGACTCAAGTCACATAGATTCGACGAAATGTTAAAAAAAGTTACGACATGATG

                                ApoI
                                DraI
                                |
                                ScaI
                                |
SmlI  SwaI  |  TatI  |
|          |  |  |  |
TGTCTCAAGATTTAAATTTTAATGCAGAGTACTTTATTGGTGTGAGGCACACAGGTAAGA
1861 -----+-----+-----+-----+-----+-----+ 1920

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ACAGAGTTCTAAATTTAAAATTACGTCTCATGAAATAACCACACTCCGTGTGTCCATTCT

      HincII                      ApoI      DraI
      |                          |          |
AGAAATGTCAACATTAAATGTATGACTTACTTGGTACAAAAATTTTTTAAAAAGGGAAC
1921 -----+-----+-----+-----+-----+-----+-----+ 1980
TCTTTACAGTTGTAATTTACATACTGAATGAACCATGTTTTTAAAAAATTTTCCCTTGA

                        Bce83I      Tth111II
                        |          SmlI |
ACCTTGACATTGTGTATTAAATGTTTACCTAAGACTATAATCTCAAGTATGATGTTTGT
1981 -----+-----+-----+-----+-----+-----+-----+ 2040
TGGAAGTGTAAACACATAATTTACAAATGGATTCTGATATTAGAGTTCATACTACAAACAA

                        BtsI
                        HaeIV
                        ApoI      Hin4I
                        |          |
TAACATATACCTCTCAAAATTTATCACCCTCAATGACACTGCATCAAAATTGACTATAA
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
ATTGTATATGGAGAGTTTTTAAATAGTGGTGAGTTACTGTGACGTAGTTTTTAACTGATATT

                        SspI                      SspI
                        |                          |
AACTAATTCAAGAAATATTTATATATATTTTTTAAATATACAAAAATATTTAGCCTGATG
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
TTGATTAAGTTCTTTATAAATATATATAAAAAATTATATGTTTTTTATAAATCGGACTAC

                        Tth111II
                        |
GAATGGCTTTCCTTTTCAAACATTATTTTCTAAGTTTCTATACAAATGAAATCTTTACCT
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
CTTACCGAAAGGAAAAGTTTGTAATAAAAGATTCAAAGATATGTTTACTTTAGAAATGGA

      MslI
      VspI                      SfcI
      |                          |
CTGCATATTAATGAGCCTTGCCATAATTACTGTAGAGTGGCTTTTCAAAGATATTTTGTT
2221 -----+-----+-----+-----+-----+-----+-----+ 2280
GACGTATAATTACTCGGAACGGTATTAATGACATCTCACCAGAAAGTTTCTATAAAACAA

                        EarI
                        SapI
                        |
GCACTAAAACTGTGGTAGTAAACTCAGTGAACATGATGTGTGGAAGAGCATAATTAGCTG
2281 -----+-----+-----+-----+-----+-----+-----+ 2340
CGTGATTTTGACACCATCATTTGAGTCACTTGTTACTACACACCTTCTCGTATTAATCGAC

      SspI                      BspMI
      |                          |
GTCAATATTTTGTCCAAAATACCTGCAAGAGTAATAAAATACATACCTTTCAAACATGA
2341 -----+-----+-----+-----+-----+-----+-----+ 2400
CAGTTATAAAAACAGGTTTTATGGACGTTCTCATTATTTTATGTATGGAAAGTTTGTACT

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Tth111II
|
TAATTATTAGTTTTTTTTTTTCTGGAACATGGATTTTGGTACATTAGCAGTAGCCT
2401 -----+-----+-----+-----+-----+-----+ 2460
ATTAATAATCAAAAAAAAAAAGGAAAGACCTTGTACCTAAAACCATGTAATCGTCATCGGA

TATTTTAATGCTTTTATGTCCTAAACATACTAATAGAAATGAAAAGACGCAGAGAGAGCAT
2461 -----+-----+-----+-----+-----+-----+ 2520
ATAAAATTACGAAATACAGGATTTGTATGATTATCTTTACTTTTCTGCGTCTCTCTCGTA

                                SpeI
                                ScaI |
                                TatI |||
                                Eco57I |
                                SfcI |
                                ApoI |
TTCGGAATACTGAAGTACTAGTTTTAGAAATGAGACTTTCAGCCAACAATCTATAGAAAG
2521 -----+-----+-----+-----+-----+-----+ 2580
AAGCCTTATGACTTCATGATCAAAATCTTTACTCTGAAAGTCGGTTGTTAGATATCTTTC

                                BsrGI
                                TatI
                                |
AATTTTATGGACCATCTTGTTTTAGTTATTTAATGTTGATGTTGTTCAAATGGGTAAATG
2581 -----+-----+-----+-----+-----+-----+ 2640
TTAAATACCTGGTAGAACAAAATCAATAAATTACAACACAAGTTTACCCATTTAC

                                ApoI
                                |
TACAGAAAGAAAATTTTAGAGTAACTTGGAACTTTGGATATAACTAGAAAAAACTAGAT
2641 -----+-----+-----+-----+-----+-----+ 2700
ATGTCTTTCTTTTAAATCTCATTGGAACCTTGAAACCTATATTGATCTTTTGTGATCTA

                                BsmI
                                |
TATAGAATTAGTCGGTAACACTTGCTAATGGACATTGGCATTTCATCTCCTTTTTCCTCCT
2701 -----+-----+-----+-----+-----+-----+ 2760
ATATCTTAATCAGCCATTGTGAACGATTACCTGTAACCGTAAGTAGAGGAAAAAGGAGGA

AAGTGTATGTATGTGTTTTAAGATTTCTGTTTTTACGATTAAAACTGGAAACATGAGGTT
2761 -----+-----+-----+-----+-----+-----+ 2820
TTCACATACATACACAAAATTCTAAAGACAAAAATGCTAATTTTGACCTTTGTACTCCAA

TTTTGTTTTTGTTTTTTTTACATAATTACATATATTCCTTCTGAATCATTTATCTTTTGAG
2821 -----+-----+-----+-----+-----+-----+ 2880
AAAACAAAAACAAAAAATGTATTAATGTATATAAGGAAGACTTAGTAAATAGAAAACCTC

                                Tth111II
                                |
                                SfcI
                                |
AAAGAAATGTTACCTAAACTTCAAATGTGCTTTTTTGTGTTGTGAGGTAATTAAATTGCTTC
2881 -----+-----+-----+-----+-----+-----+ 2940
TTTCTTTACAATGGATTTGAAGTTTACACGAAAAACAAACACTCCATTAATTTAACGAAG

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